

Abstract

The connectron structure of a genome determines sets of four DNA sequences of minimum length of 15-bases (C1 and C2 which are in the 3'UTR of a gene, T1 which is on the 5'-side and T2 which is on the 3'-side of a set of genes). The connectron state of a genome provides information that makes it possible to decide where and how connectrons can be deleted from the native genome or added to the native genome to modify genomic gene expression behavior.